

1644



1600

RAW SEQUENCE LISTING
 PATENT APPLICATION: US/09/728,421E

DATE: 11/18/2002
 TIME: 12:51:17

P#22

Input Set : A:\09.728.421.txt
 Output Set: N:\CRF4\11182002\I728421E.raw

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NOV 29 2002

TECH CENTER 1600/2900

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3 <110> APPLICANT: Yoshinaga, Steven K.
 4 Mak, Tak Wah
 5 Shahinian, Arda
 6 Trafuri Bladt, Anna
 7 Senaldi, Giorgio
 9 <120> TITLE OF INVENTION: Novel Polypeptides Involved in Immune Response
 11 <130> FILE REFERENCE: 6843.0050-03
 13 <140> CURRENT APPLICATION NUMBER: 09/728,421E
 14 <141> CURRENT FILING DATE: 2000-11-28
 16 <150> PRIOR APPLICATION NUMBER: PCT/US00/01871
 17 <151> PRIOR FILING DATE: 2000-01-27
 19 <150> PRIOR APPLICATION NUMBER: US 09/264,527
 20 <151> PRIOR FILING DATE: 1999-03-08
 22 <150> PRIOR APPLICATION NUMBER: US 09/244,448
 23 <151> PRIOR FILING DATE: 1999-02-03
 25 <160> NUMBER OF SEQ ID NOS: 39
 27 <170> SOFTWARE: PatentIn version 3.1
 29 <210> SEQ ID NO: 1
 30 <211> LENGTH: 600
 31 <212> TYPE: DNA
 32 <213> ORGANISM: Mus musculus
 34 <220> FEATURE:
 35 <221> NAME/KEY: CDS
 36 <222> LOCATION: (1)..(600)
 37 <223> OTHER INFORMATION:

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41 Met Lys Pro Tyr Phe Cys Arg Val Phe Val Phe Cys Phe Leu Ile Arg	
42 1 5 10 15	
44 ctt tta aca gga gaa atc aat ggc tcg gcc gat cat agg atg ttt tca	96
45 Leu Leu Thr Gly Glu Ile Asn Gly Ser Ala Asp His Arg Met Phe Ser	
46 20 25 30	
48 ttt cac aat gga ggt gta cag att tct tgt aaa tac cct gag act gtc	144
49 Phe His Asn Gly Gly Val Gln Ile Ser Cys Lys Tyr Pro Glu Thr Val	
50 35 40 45	
52 cag cag tta aaa atg cga ttg ttc aga gag aga gaa gtc ctc tgc gaa	192
53 Gln Gln Leu Lys Met Arg Leu Phe Arg Glu Arg Glu Val Leu Cys Glu	
54 50 55 60	
56 ctc acc aag acc aag gga agc gga aat gcg gtg tcc atc aag aat cca	240
57 Leu Thr Lys Thr Lys Gly Ser Gly Asn Ala Val Ser Ile Lys Asn Pro	
58 65 70 75 80	
60 atg ctc tgt cta tat cat ctg tca aac aac agc gtc tct ttt ttc cta	288
61 Met Leu Cys Leu Tyr His Leu Ser Asn Asn Ser Val Ser Phe Phe Leu	

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62          85          90          95
64 aac aac cca gac agc tcc cag gga agc tat tac ttc tgc agc ctg tcc 336
65 Asn Asn Pro Asp Ser Ser Gln Gly Ser Tyr Tyr Phe Cys Ser Leu Ser
66          100          105          110
68 att ttt gac cca cct cct ttt caa gaa agg aac ctt agt gga gga tat 384
69 Ile Phe Asp Pro Pro Pro Phe Gln Glu Arg Asn Leu Ser Gly Gly Tyr
70          115          120          125
72 ttg cat att tat gaa tcc cag ctc tgc tgc cag ctg aag ctc tgg cta 432
73 Leu His Ile Tyr Glu Ser Gln Leu Cys Cys Gln Leu Lys Leu Trp Leu
74          130          135          140
76 ccc gta ggg tgt gca gct ttc gtt gtg gta ctc ctt ttt gga tgc ata 480
77 Pro Val Gly Cys Ala Ala Phe Val Val Val Leu Leu Phe Gly Cys Ile
78 145          150          155          160
80 ctt atc atc tgg ttt tca aaa aag aaa tac gga tcc agt gtg cat gac 528
81 Leu Ile Ile Trp Phe Ser Lys Lys Lys Tyr Gly Ser Ser Val His Asp
82          165          170          175
84 cct aat agt gaa tac atg ttc atg gcg gca gtc aac aca aac aaa aag 576
85 Pro Asn Ser Glu Tyr Met Phe Met Ala Ala Val Asn Thr Asn Lys Lys
86          180          185          190
88 tct aga ctt gca ggt gtg acc tca 600
89 Ser Arg Leu Ala Gly Val Thr Ser
90          195          200
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94 <211> LENGTH: 200
95 <212> TYPE: PRT
96 <213> ORGANISM: Mus musculus
98 <400> SEQUENCE: 2
100 Met Lys Pro Tyr Phe Cys Arg Val Phe Val Phe Cys Phe Leu Ile Arg
101 1          5          10          15
104 Leu Leu Thr Gly Glu Ile Asn Gly Ser Ala Asp His Arg Met Phe Ser
105          20          25          30
108 Phe His Asn Gly Gly Val Gln Ile Ser Cys Lys Tyr Pro Glu Thr Val
109          35          40          45
112 Gln Gln Leu Lys Met Arg Leu Phe Arg Glu Arg Glu Val Leu Cys Glu
113          50          55          60
116 Leu Thr Lys Thr Lys Gly Ser Gly Asn Ala Val Ser Ile Lys Asn Pro
117 65          70          75          80
120 Met Leu Cys Leu Tyr His Leu Ser Asn Asn Ser Val Ser Phe Phe Leu
121          85          90          95
124 Asn Asn Pro Asp Ser Ser Gln Gly Ser Tyr Tyr Phe Cys Ser Leu Ser
125          100          105          110
128 Ile Phe Asp Pro Pro Pro Phe Gln Glu Arg Asn Leu Ser Gly Gly Tyr
129          115          120          125
132 Leu His Ile Tyr Glu Ser Gln Leu Cys Cys Gln Leu Lys Leu Trp Leu
133          130          135          140
136 Pro Val Gly Cys Ala Ala Phe Val Val Val Leu Leu Phe Gly Cys Ile
137 145          150          155          160
140 Leu Ile Ile Trp Phe Ser Lys Lys Lys Tyr Gly Ser Ser Val His Asp
141          165          170          175

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144 Pro Asn Ser Glu Tyr Met Phe Met Ala Ala Val Asn Thr Asn Lys Lys
145           180           185           190
148 Ser Arg Leu Ala Gly Val Thr Ser
149           195           200
152 <210> SEQ ID NO: 3
153 <211> LENGTH: 200
154 <212> TYPE: PRT
155 <213> ORGANISM: Mus musculus
157 <400> SEQUENCE: 3
159 Met Lys Pro Tyr Phe Cys Arg Val Phe Val Phe Cys Phe Leu Ile Arg
160 1           5           10           15
163 Leu Leu Thr Gly Glu Ile Asn Gly Ser Ala Asp His Arg Met Phe Ser
164           20           25           30
167 Phe His Asn Gly Gly Val Gln Ile Ser Cys Lys Tyr Pro Glu Thr Val
168           35           40           45
171 Gln Gln Leu Lys Met Arg Leu Phe Arg Glu Arg Glu Val Leu Cys Glu
172           50           55           60
175 Leu Thr Lys Thr Lys Gly Ser Gly Asn Ala Val Ser Ile Lys Asn Pro
176 65           70           75           80
179 Met Leu Cys Leu Tyr His Leu Ser Asn Asn Ser Val Ser Phe Phe Leu
180           85           90           95
183 Asn Asn Pro Asp Ser Ser Gln Gly Ser Tyr Tyr Phe Cys Ser Leu Ser
184           100          105          110
187 Ile Phe Asp Pro Pro Pro Phe Gln Glu Arg Asn Leu Ser Gly Gly Tyr
188           115          120          125
191 Leu His Ile Tyr Glu Ser Gln Leu Cys Cys Gln Leu Lys Leu Trp Leu
192           130          135          140
195 Pro Val Gly Cys Ala Ala Phe Val Val Val Leu Leu Phe Gly Cys Ile
196 145          150          155          160
199 Leu Ile Ile Trp Phe Ser Lys Lys Lys Tyr Gly Ser Ser Val His Asp
200           165          170          175
203 Pro Asn Ser Glu Tyr Met Phe Met Ala Ala Val Asn Thr Asn Lys Lys
204           180          185          190
207 Ser Arg Leu Ala Gly Val Thr Ser
208           195          200
211 <210> SEQ ID NO: 4
212 <211> LENGTH: 218
213 <212> TYPE: PRT
214 <213> ORGANISM: Mus musculus
216 <400> SEQUENCE: 4
218 Met Thr Leu Arg Leu Leu Phe Leu Ala Leu Asn Phe Phe Ser Val Gln
219 1           5           10           15
222 Val Thr Glu Asn Lys Ile Leu Val Lys Gln Ser Pro Leu Leu Val Val
223           20           25           30
226 Asp Ser Asn Glu Val Ser Leu Ser Cys Arg Tyr Ser Tyr Asn Leu Leu
227           35           40           45
230 Ala Lys Glu Phe Arg Ala Ser Leu Tyr Lys Gly Val Asn Ser Asp Val
231           50           55           60
234 Glu Val Cys Val Gly Asn Gly Asn Phe Thr Tyr Gln Pro Gln Phe Arg

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235 65          70          75          80
238 Ser Asn Ala Glu Phe Asn Cys Asp Gly Asp Phe Asp Asn Glu Thr Val
239          85          90          95
242 Thr Phe Arg Leu Trp Asn Leu His Val Asn His Thr Asp Ile Tyr Phe
243          100          105          110
246 Cys Lys Ile Glu Phe Met Tyr Pro Pro Pro Tyr Leu Asp Asn Glu Arg
247          115          120          125
250 Ser Asn Gly Thr Ile Ile His Ile Lys Glu Lys His Leu Cys His Thr
251          130          135          140
254 Gln Ser Ser Pro Lys Leu Phe Trp Ala Leu Val Val Val Ala Gly Val
255 145          150          155          160
258 Leu Phe Cys Tyr Gly Leu Leu Val Thr Val Ala Leu Cys Val Ile Trp
259          165          170          175
262 Thr Asn Ser Arg Arg Asn Arg Leu Leu Gln Val Thr Thr Met Asn Met
263          180          185          190
266 Thr Pro Arg Arg Pro Gly Leu Thr Arg Lys Pro Tyr Gln Pro Tyr Ala
267          195          200          205
270 Pro Ala Arg Asp Phe Ala Ala Tyr Arg Pro
271          210          215

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274 <210> SEQ ID NO: 5

275 <211> LENGTH: 44

276 <212> TYPE: PRT

277 <213> ORGANISM: Artificial sequence

279 <220> FEATURE:

280 <223> OTHER INFORMATION: Synthetic

282 <400> SEQUENCE: 5

284 Met Arg Leu Leu Val Ser Cys Tyr Leu Val Cys Cys Asn Val Phe Leu

285 1 5 10 15

288 Asn Tyr Phe Cys Pro Pro Pro Ser Gly His Ile Glu Leu Cys Lys Leu

289 20 25 30

292 Trp Leu Val Phe Leu Leu Leu Ile Trp Pro Arg Ala

293 35 40

296 <210> SEQ ID NO: 6

297 <211> LENGTH: 966

298 <212> TYPE: DNA

299 <213> ORGANISM: Mus musculus

301 <220> FEATURE:

302 <221> NAME/KEY: CDS

303 <222> LOCATION: (1)..(966)

304 <223> OTHER INFORMATION:

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308 Met Gln Leu Lys Cys Pro Cys Phe Val Ser Leu Gly Thr Arg Gln Pro

309 1 5 10 15

311 gtt tgg aag aag ctc cat gtt tct agc ggg ttc ttt tct ggt ctt ggt 96

312 Val Trp Lys Lys Leu His Val Ser Ser Gly Phe Phe Ser Gly Leu Gly

313 20 25 30

315 ctg ttc ttg ctg ctg ttg agc agc ctc tgt gct gcc tct gca gag act 144

316 Leu Phe Leu Leu Leu Leu Ser Ser Leu Cys Ala Ala Ser Ala Glu Thr

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317	35	40	45	
319	gaa gtc ggt gca atg gtg ggc agc aat gtg gtg ctg agc tgc att gac	192		
320	Glu Val Gly Ala Met Val Gly Ser Asn Val Val Leu Ser Cys Ile Asp			
321	50 55 60			
323	ccc cac aga cgc cat ttc aac ttg agt ggt ctg tat gtc tat tgg caa	240		
324	Pro His Arg Arg His Phe Asn Leu Ser Gly Leu Tyr Val Tyr Trp Gln			
325	65 70 75 80			
327	atc gaa aac cca gaa gtt tcg gtg act tac tac ctg cct tac aag tct	288		
328	Ile Glu Asn Pro Glu Val Ser Val Thr Tyr Tyr Leu Pro Tyr Lys Ser			
329	85 90 95			
331	cca ggg atc aat gtg gac agt tcc tac aag aac agg ggc cat ctg tcc	336		
332	Pro Gly Ile Asn Val Asp Ser Ser Tyr Lys Asn Arg Gly His Leu Ser			
333	100 105 110			
335	ctg gac tcc atg aag cag ggt aac ttc tct ctg tac ctg aag aat gtc	384		
336	Leu Asp Ser Met Lys Gln Gly Asn Phe Ser Leu Tyr Leu Lys Asn Val			
337	115 120 125			
339	acc cct cag gat acc cag gag ttc aca tgc cgg gta ttt atg aat aca	432		
340	Thr Pro Gln Asp Thr Gln Glu Phe Thr Cys Arg Val Phe Met Asn Thr			
341	130 135 140			
343	gcc aca gag tta gtc aag atc ttg gaa gag gtg gtc agg ctg cgt gtg	480		
344	Ala Thr Glu Leu Val Lys Ile Leu Glu Glu Val Val Arg Leu Arg Val			
345	145 150 155 160			
347	gca gca aac ttc agt aca cct gtc atc agc acc tct gat agc tcc aac	528		
348	Ala Ala Asn Phe Ser Thr Pro Val Ile Ser Thr Ser Asp Ser Ser Asn			
349	165 170 175			
351	ccg ggc cag gaa cgt acc tac acc tgc atg tcc aag aat ggc tac cca	576		
352	Pro Gly Gln Glu Arg Thr Tyr Thr Cys Met Ser Lys Asn Gly Tyr Pro			
353	180 185 190			
355	gag ccc aac ctg tat tgg atc aac aca acg gac aat agc cta ata gac	624		
356	Glu Pro Asn Leu Tyr Trp Ile Asn Thr Thr Asp Asn Ser Leu Ile Asp			
357	195 200 205			
359	acg gct ctg cag aat aac act gtc tac ttg aac aag ttg ggc ctg tat	672		
360	Thr Ala Leu Gln Asn Asn Thr Val Tyr Leu Asn Lys Leu Gly Leu Tyr			
361	210 215 220			
363	gat gta atc agc aca tta agg ctg cct tgg aca tct cgt ggg gat gtt	720		
364	Asp Val Ile Ser Thr Leu Arg Leu Pro Trp Thr Ser Arg Gly Asp Val			
365	225 230 235 240			
367	ctg tgc tgc gta gag aat gtg gct ctg cac cag aac atc act agc att	768		
368	Leu Cys Cys Val Glu Asn Val Ala Leu His Gln Asn Ile Thr Ser Ile			
369	245 250 255			
371	agc cag gca gaa agt ttc act gga aat aac aca aag aac cca cag gaa	816		
372	Ser Gln Ala Glu Ser Phe Thr Gly Asn Asn Thr Lys Asn Pro Gln Glu			
373	260 265 270			
375	acc cac aat aat gag tta aaa gtc ctt gtc ccc gtc ctt gct gta ctg	864		
376	Thr His Asn Asn Glu Leu Lys Val Leu Val Pro Val Leu Ala Val Leu			
377	275 280 285			
379	gcg gca gcg gca ttc gtt tcc ttc atc ata tac aga cgc acg cgt ccc	912		
380	Ala Ala Ala Ala Phe Val Ser Phe Ile Ile Tyr Arg Arg Thr Arg Pro			
381	290 295 300			

RAW SEQUENCE LISTING ERROR SUMMARY
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Invalid <213> Response:

Use of "Artificial" only as "<213> Organism" response is incomplete,
per 1.823(b) of New Sequence Rules. Valid response is Artificial Sequence.

Seq#:36,37,38,39

VERIFICATION SUMMARY

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Input Set : A:\09.728.421.txt

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L:39 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:1,Line#:37
L:306 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:6,Line#:304
L:701 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:11,Line#:699
L:1065 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:16,Line#:1058
L:1065 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:16,Line#:1063
L:1468 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:21
L:1477 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:21,Line#:1470
L:1477 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:21,Line#:1475